



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Gorman, Daniel M.
Randall, Troy D.
Zlotnik, Albert
- (ii) TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED REAGENTS
- (iii) NUMBER OF SEQUENCES: 9
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DNAX Research Institute
 - (B) STREET: 901 California Avenue
 - (C) CITY: Palo Alto
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94304-1104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/911,423
 - (B) FILING DATE: 14-AUG-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/023,419
 - (B) FILING DATE: 16-AUG-1996
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/027,901
 - (B) FILING DATE: 07-OCT-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ching, Edwin P.
 - (B) REGISTRATION NUMBER: 34,090
 - (C) REFERENCE/DOCKET NUMBER: DX0612K
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 650-852-9196
 - (B) TELEFAX: 650-496-1200

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1073 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 68..751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CTCGAGATCC ATTGTGCTGG AAAGGGA	ACT CCTGAAATCA GCCGACAGAA GACTCAGGAG	60
AAGCACT ATG GGG GCA TGG GCC ATG CTG TAT GGA GTC TCG ATG CTC TGT		109
Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys		
1 5 10		
GTG CTG GAC CTA GGT CAG CCG AGT GTA GTT GAG GAG CCT GGC TGT GGC		157
Val Leu Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly		
15 20 25 30		
CCT GGC AAG GTT CAG AAC GGA AGT GGC AAC AAC ACT CGC TGC TGC AGC		205
Pro Gly Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser		
35 40 45		
CTG TAT GCT CCA GGC AAG GAG GAC TGT CCA AAA GAA AGG TGC ATA TGT		253
Leu Tyr Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys		
50 55 60		
GTC ACA CCT GAG TAC CAC TGT GGA GAC CCT CAG TGC AAG ATC TGC AAG		301
Val Thr Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys		
65 70 75		
CAC TAC CCC TGC CAA CCA GGC CAG AGG GTG GAG TCT CAA GGG GAT ATT		349
His Tyr Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile		
80 85 90		
GTG TTT GGC TTC CGG TGT GTT GCC TGT GCC ATG GGC ACC TTC TCC GCA		397
Val Phe Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala		
95 100 105 110		
GGT CGT GAC GGT CAC TGC AGA CTT TGG ACC AAC TGT TCT CAG TTT GGA		445
Gly Arg Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly		
115 120 125		
TTT CTC ACC ATG TTC CCT GGG AAC AAG ACC CAC AAT GCT GTG TGC ATC		493
Phe Leu Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile		
130 135 140		
CCG GAG CCA CTG CCC ACT GAG CAA TAC GGC CAT TTG ACT GTC ATC TTC		541
Pro Glu Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe		
145 150 155		
CTG GTC ATG GCT GCA TGC ATT TTC TTC CTA ACC ACA GTC CAG CTC GGC		589
Leu Val Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly		
160 165 170		

CTG CAC ATA TGG CAG CTG AGG AGG CAA CAC ATG TGT CCC CGA GAG ACC	637
Leu His Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr	
175 180 185 190	
CAG CCA TTC GCG GAG GTG CAG TTG TCA GCT GAG GAT GCT TGC AGC TTC	685
Gln Pro Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe	
195 200 205	
CAG TTC CCT GAG GAG GAA CGC GGG GAG CAG ACA GAA GAA AAG TGT CAT	733
Gln Phe Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His	
210 215 220	
CTG GGG GGT CGG TGG CCA TGAGGCCTGG TCTTCCTCTG TGCCCCAAGC	781
Leu Gly Gly Arg Trp Pro	
225	
CAGACGCTAC AAGACTTGCC CAGCTATAACC CTTGGTGAGA GCAGGGGCCA TGCTCTGCAC	841
CCTTCCCTGG GCCTGGCCCT GCTCCCCTCA ACAGTGGCGG AAGTGGGTGT ATGAGAGCGG	901
TGAGTTACGA TTGGGCCCTA TGGCTGCCTT TCTCATTTGA CAGCTCTGTT GGAGTAGGGT	961
CTTTGGGGCCC ACCAAGAGCA CCACGTTTAG CACAAGATCT TGTACAAGAA TAAATACTTG	1021
TTTAGTAACC TGAAAAAAAAA AAAAAAAGG GCGGCCGCGG AGGCCGAATT CC	1073

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 228 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Ala Trp Ala Met Leu Tyr Gly Val Ser Met Leu Cys Val Leu	
1 5 10 15	
Asp Leu Gly Gln Pro Ser Val Val Glu Glu Pro Gly Cys Gly Pro Gly	
20 25 30	
Lys Val Gln Asn Gly Ser Gly Asn Asn Thr Arg Cys Cys Ser Leu Tyr	
35 40 45	
Ala Pro Gly Lys Glu Asp Cys Pro Lys Glu Arg Cys Ile Cys Val Thr	
50 55 60	
Pro Glu Tyr His Cys Gly Asp Pro Gln Cys Lys Ile Cys Lys His Tyr	
65 70 75 80	
Pro Cys Gln Pro Gly Gln Arg Val Glu Ser Gln Gly Asp Ile Val Phe	
85 90 95	

Gly Phe Arg Cys Val Ala Cys Ala Met Gly Thr Phe Ser Ala Gly Arg
 100 105 110
 Asp Gly His Cys Arg Leu Trp Thr Asn Cys Ser Gln Phe Gly Phe Leu
 115 120 125
 Thr Met Phe Pro Gly Asn Lys Thr His Asn Ala Val Cys Ile Pro Glu
 130 135 140
 Pro Leu Pro Thr Glu Gln Tyr Gly His Leu Thr Val Ile Phe Leu Val
 145 150 155 160
 Met Ala Ala Cys Ile Phe Phe Leu Thr Thr Val Gln Leu Gly Leu His
 165 170 175
 Ile Trp Gln Leu Arg Arg Gln His Met Cys Pro Arg Glu Thr Gln Pro
 180 185 190
 Phe Ala Glu Val Gln Leu Ser Ala Glu Asp Ala Cys Ser Phe Gln Phe
 195 200 205
 Pro Glu Glu Glu Arg Gly Glu Gln Thr Glu Glu Lys Cys His Leu Gly
 210 215 220
 Gly Arg Trp Pro
 225

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1006 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..723

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATG GCA CAG CAC GGG GCG ATG GGC GCG TTT CGG GCC CTG TGC GGC CTG	48
Met Ala Gln His Gly Ala Met Gly Ala Phe Arg Ala Leu Cys Gly Leu	
1 5 10 15	
GCG CTG CTG TGC GCG CTC AGC CTG GGT CAG CGC CCC ACC GGG GGT CCC	96
Ala Leu Leu Cys Ala Leu Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro	
20 25 30	
GGG TGC GGC CCT GGG CGC CTC CTG CTT GGG ACG GGA ACG GAC GCG CGC	144
Gly Cys Gly Pro Gly Arg Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg	
35 40 45	

TGC TGC CGG GTT CAC ACG ACG CGC TGC TGC CGC GAT TAC CCG GGC GAG Cys Cys Arg Val His Thr Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu 50 55 60	192
GAG TGC TGT TCC GAG TGG GAC TGC ATG TGT GTC CAG CCT GAA TTC CAC Glu Cys Cys Ser Glu Trp Asp Cys Met Cys Val Gln Pro Glu Phe His 65 70 75 80	240
TGC GGA GAC CCT TGC TGC ACG ACC TGC CGG CAC CAC CCT TGT CCC CCA Cys Gly Asp Pro Cys Cys Thr Thr Cys Arg His His Pro Cys Pro Pro 85 90 95	288
GGC CAG GGG GTA CAG TCC CAG GGG AAA TTC AGT TTT GGC TTC CAG TGT Gly Gln Gly Val Gln Ser Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys 100 105 110	336
ATC GAC TGT GCC TCG GGG ACC TTC TCC GGG GGC CAC GAA GGC CAC TGC Ile Asp Cys Ala Ser Gly Thr Phe Ser Gly Gly His Glu Gly His Cys 115 120 125	384
AAA CCT TGG ACA GAC TGC ACC CAG TTC GGG TTT CTC ACT GTG TTC CCT Lys Pro Trp Thr Asp Cys Thr Gln Phe Gly Phe Leu Thr Val Phe Pro 130 135 140	432
GGG AAC AAG ACC CAC AAC GCT GTG TGC GTC CCA GGG TCC CCG CCG GCA Gly Asn Lys Thr His Asn Ala Val Cys Val Pro Gly Ser Pro Pro Ala 145 150 155 160	480
GAG CCG CTT GGG TGG CTG ACC GTC GTC CTC CTG GCC GTG GCC GCC TGC Glu Pro Leu Gly Trp Leu Thr Val Val Leu Leu Ala Val Ala Ala Cys 165 170 175	528
GTC CTC CTC CTG ACC TCG GCC CAG CTT GGA CTG CAC ATC TGG CAG CTG Val Leu Leu Leu Thr Ser Ala Gln Leu Gly Leu His Ile Trp Gln Leu 180 185 190	576
AGG AGT CAG TGC ATG TGG CCC CGA GAG ACC CAG CTG CTG CTG GAG GTG Arg Ser Gln Cys Met Trp Pro Arg Glu Thr Gln Leu Leu Leu Glu Val 195 200 205	624
CCG CCG TCG ACC GAA GAC GCC AGA AGC TGC CAG TTC CCC GAG GAA GAG Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro Glu Glu Glu 210 215 220	672
CGG GGC GAG CGA TCG GCA GAG GAG AAG GGG CGG CTG GGA GAC CTG TGG Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp 225 230 235 240	720
GTG TGAGCCTGGC CGTCCTCCGG GGCCACCGAC CGCAGCCAGC CCCTCCCCAG Val	773
GAGCTCCCCA GGCCGCAGGG GCTCTGCGTT CTGCTCTGGG CCGGGCCCTG CTCCCCTGGC	833
AGCAGAAGTG GGTGCAGGAA GGTGGCAGTG ACCAGCGCCC TGGACCATGC AGTTCGGCGG	893
CCGCTCTAAA GGATCCAAGC TTACGTACGC GTGCATGCGA CGTCATAGCT CTTCTATAGT	953

GTCACCTAAA TTCAATTCAC TGGCCGTCGT TTTACAACGT CCTGACTGGG AAA

(2) INFORMATION FOR SEQ ID NO:4:

(A) LENGTH: 241 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly Asp Leu Trp
 225 230 235 240

Val

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 723 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATGGCNCARC AYGGNGCNAT GGGNGCNTTY MGNGCNYTNT GYGGNYTNGC NYTNYTNTGY	60
GCNYTNWSNY TNGGNCARMG NCCNACNGGN GGNCNGGNT GYGGNCCNGG NMGNYTNYTN	120
YTNGGNACNG GNACNGAYGC NMGNTGYTGY MGNGTNCAYA CNACNMGNTG YTGyMGNGAY	180
TAYCCNGGNG ARGARTGYTG YWSNGARTGG GAYTGYATGT GYGTNCARCC NGARTTYCAY	240
TGYGGNGAYC CNTGYTGYAC NACNTGYMGN CAYCAYCCNT GYCCNCCNGG NCARGGNGTN	300
CARWSNCARG GNAARTTYWS NTTYGGNTTY CARTGYATHG AYTGYGCNWS NGGNACNTTY	360
WSNGGNGGNC AYGARGGNCA YTGyAARCCN TGGACNGAYT GYACNCARTT YGGNTTYTYTN	420
ACNGTNTTYC CNGGNAAYAA RACNCAYAA YGCNGTNTGYG TNCCNGGNWS NCCNCCNGCN	480
GARCCNYTNG GNTGGYTAC NGTNGTNYTN YTNGCNGTNG CNGCNTGYGT NYTNYTNYTN	540
ACNWSNGCNC ARYTNGGNYT NCAYATHTGG CARYTNMGW SNCARTGYAT GTGGCCNMGN	600
GARACNCARY TNYTNYTNGA RGTNCCNCCN WSNACNGARG AYGCNMGNWS NTGYCARTTY	660
CCNGARGARG ARMGNGGNGA RMGNWSNGCN GARGARAARG GNMGNYTNGG NGAYYTNTGG	720
GTN	723

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 228 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Ala Phe Arg Ala Leu Cys Gly Leu Ala Leu Leu Cys Ala Leu
1 5 10 15
Ser Leu Gly Gln Arg Pro Thr Gly Gly Pro Gly Cys Gly Pro Gly Arg
20 25 30
Leu Leu Leu Gly Thr Gly Thr Asp Ala Arg Cys Cys Arg Val His Thr
35 40 45
Thr Arg Cys Cys Arg Asp Tyr Pro Gly Glu Glu Cys Cys Ser Glu Trp
50 55 60
Asp Cys Met Cys Val Gln Pro Glu Phe His Cys Gly Asp Pro Cys Cys
65 70 75 80
Thr Thr Cys Arg His His Pro Cys Pro Pro Gly Gln Gly Val Gln Ser
85 90 95
Gln Gly Lys Phe Ser Phe Gly Phe Gln Cys Ile Asp Cys Ala Ser Gly
100 105 110
Thr Phe Ser Gly Gly His Glu Gly His Cys Lys Pro Trp Thr Asp Cys
115 120 125
Thr Gln Phe Gly Phe Leu Thr Val Phe Pro Gly Asn Lys Thr His Asn
130 135 140
Ala Val Cys Val Pro Gly Ser Pro Pro Ala Glu Pro Leu Gly Trp Leu
145 150 155 160
Thr Val Val Leu Leu Ala Val Ala Ala Cys Val Leu Leu Leu Thr Ser
165 170 175
Ala Gln Leu Gly Leu His Ile Trp Gln Leu Arg Lys Thr Gln Leu Leu
180 185 190
Leu Glu Val Pro Pro Ser Thr Glu Asp Ala Arg Ser Cys Gln Phe Pro
195 200 205
Glu Glu Glu Arg Gly Glu Arg Ser Ala Glu Glu Lys Gly Arg Leu Gly
210 215 220
Asp Leu Trp Val
225

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 232 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Gly	Ala	Phe	Arg	Ala	Leu	Cys	Gly	Leu	Ala	Leu	Leu	Cys	Ala	Leu	
1				5					10					15		
Ser	Leu	Gly	Gln	Arg	Pro	Thr	Gly	Gly	Pro	Gly	Cys	Gly	Pro	Gly	Arg	
			20					25					30			
Leu	Leu	Leu	Gly	Thr	Gly	Thr	Asp	Ala	Arg	Cys	Cys	Arg	Val	His	Thr	
		35					40					45				
Thr	Arg	Cys	Cys	Arg	Asp	Tyr	Pro	Gly	Glu	Glu	Cys	Cys	Ser	Glu	Trp	
	50					55					60					
Asp	Cys	Met	Cys	Val	Gln	Pro	Glu	Phe	His	Cys	Gly	Asp	Pro	Cys	Cys	
65					70					75					80	
Thr	Thr	Cys	Arg	His	His	Pro	Cys	Pro	Pro	Gly	Gln	Gly	Val	Gln	Ser	
				85					90					95		
Gln	Gly	Lys	Ser	Trp	Arg	Cys	Leu	Trp	Glu	Ser	Thr	Gln	Ala	Arg	Gly	
			100					105					110			
Ser	Thr	Arg	Ala	Arg	Gly	Arg	Ala	Arg	Gly	His	Arg	Cys	Pro	Ala	Arg	
		115					120					125				
Thr	Cys	Gly	Val	Trp	Gly	Pro	Glu	Ser	Cys	Glu	Ala	Gly	Gln	Ala	Arg	
	130					135					140					
Pro	Cys	Ser	Gly	Thr	Thr	Gly	His	Glu	Ala	Leu	Gly	Val	Ser	Cys	Pro	
145					150					155					160	
Cys	Phe	Leu	Ser	Leu	Gly	Phe	Ser	Ile	Gln	His	Glu	Gly	Cys	Glu	Asn	
				165				170						175		
Pro	Ala	Gly	Arg	Trp	Gly	Arg	Val	Pro	Gly	Ala	Val	Trp	Leu	Ser	Gly	
			180					185					190			
Pro	Gly	His	Pro	Ser	Cys	Leu	Ser	Ser	Pro	His	Thr	Glu	Arg	Ala	Cys	
		195					200					205				
Pro	Val	Pro	Pro	Gly	Val	Leu	Ser	Gly	Ala	Trp	Gly	Cys	Thr	Leu	Phe	
	210					215					220					
Trp	Lys	Glu	Gln	Leu	Lys	Ser	Ser									
225					230											

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 311 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Gly	Ala	Phe	Arg	Ala	Leu	Cys	Gly	Leu	Ala	Leu	Leu	Cys	Ala	Leu	1	5	10	15
Ser	Leu	Gly	Gln	Arg	Pro	Thr	Gly	Gly	Pro	Gly	Cys	Gly	Pro	Gly	Arg	20	25	30	
Leu	Leu	Leu	Gly	Thr	Gly	Thr	Asp	Ala	Arg	Cys	Cys	Arg	Val	His	Thr	35	40	45	
Thr	Arg	Cys	Cys	Arg	Asp	Tyr	Pro	Gly	Glu	Glu	Cys	Cys	Ser	Glu	Trp	50	55	60	
Asp	Cys	Met	Cys	Val	Gln	Pro	Glu	Phe	His	Cys	Gly	Asp	Pro	Cys	Cys	65	70	75	80
Thr	Thr	Cys	Arg	His	His	Pro	Cys	Pro	Pro	Gly	Gln	Gly	Val	Gln	Ser	85	90	95	
Gln	Gly	Lys	Phe	Ser	Phe	Gly	Phe	Gln	Cys	Ile	Asp	Cys	Ala	Ser	Gly	100	105	110	
Thr	Phe	Ser	Gly	Gly	His	Glu	Gly	His	Cys	Lys	Pro	Trp	Thr	Asp	Cys	115	120	125	
Thr	Gln	Phe	Gly	Phe	Leu	Thr	Val	Phe	Pro	Gly	Asn	Lys	Thr	His	Asn	130	135	140	
Ala	Val	Cys	Val	Pro	Gly	Ser	Pro	Pro	Ala	Glu	Pro	Leu	Gly	Trp	Leu	145	150	155	160
Thr	Val	Val	Leu	Leu	Ala	Val	Ala	Ala	Cys	Val	Leu	Leu	Leu	Thr	Ser	165	170	175	
Ala	Gln	Leu	Gly	Leu	His	Ile	Trp	Gln	Leu	Arg	Ser	Gln	Cys	Met	Trp	180	185	190	
Pro	Arg	Gly	Leu	Ser	Gln	Pro	Gly	Ala	Gly	Arg	Trp	Glu	His	Gly	Cys	195	200	205	
Leu	Leu	Thr	Val	Ala	Pro	Leu	Gln	Arg	Pro	Ser	Cys	Cys	Trp	Arg	Cys	210	215	220	
Arg	Arg	Arg	Pro	Lys	Thr	Pro	Glu	Ala	Ala	Ser	Ser	Pro	Arg	Lys	Ser	225	230	235	240
Gly	Ala	Ser	Asp	Arg	Gln	Arg	Arg	Arg	Gly	Gly	Trp	Glu	Thr	Cys	Gly				

